

SEQUENCE LISTING

<110> DYAX Corp.
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Luneau, Christopher J.
Ladner, Robert C

<120> NOVEL ENTEROKINASE CLEAVAGE SEQUENCES

<130> DYX-012.1 US, DYX-012.1 PCT

<140> not yet assigned
<141> 2001-06-19

<150> US 09/597,321
<151> 2000-06-19

<160> 217

<170> PatentIn version 3.1

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 35 40 45

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Glu His Leu Phe Asp Arg Met
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Ser Gly Gly Asp Asp Arg Met
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Ser Leu Asp Asp Asp Arg Thr

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<211> 7

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Asp Val Tyr Ser Glu Arg Met

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Asn Met Asp Trp Asp Arg Ser

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Asn Val Arg Met Asp Arg Ser

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Ser His Arg Asp Glu Lys Val

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<400> 166

TOBT90" 29248850

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Phe Val Met Asn Asp Lys Gly
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His Ala Ile Glu Glu Arg Ser
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Gly Ser Gly Gly Glu Arg Thr
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Ala Val Ile Gly Asp Arg Ser
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Ser Gly Gly Glu Glu Arg Gly
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Val Glu Phe Tyr Asp Arg Met
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Ser Leu Asp Asp Asp Arg Thr
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Ser Gly Gly Gln Glu Arg Ser
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<400> 179

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Asp His Val Trp Asp Arg Ala
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Gly Ser Gly Gly Asp Arg Ile
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Ile Glu Asp Glu Asp Arg Ala
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<211> 7

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Met Thr Phe Asp Glu Arg Gly
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Gly Asp Trp Asp Asp Lys Asn
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Ile Ala Tyr Gln Asp Arg Met
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Gly Ser Gly Gly Asp Arg Ile
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Gly Phe Val Gln Glu Arg Met
1 5

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Asp Ile Asn Asp Asp Arg Ser
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Gly Trp Asn Asp Asp Arg Ile
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Gly Gly Phe Glu Asp Arg Leu
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Gly Ser Gly Gly Asp Arg Asn
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<210> 192
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<212> PRT
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Ala Ala Val Glu Asp Arg Asn
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Asp Tyr Arg Leu Asp Arg Ile
1 5

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<400> 194

Gly Asp Asp Asp Asp Lys Ile
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Asp Arg Met Tyr Gln Leu Asp Lys Thr Gly Phe Met Ile
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<210> 196
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<210> 197

<211> 9

<212> PRT

<213> natural enterokinase cleavage sequence

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<213> negative control in EK cleavage experiment

<400> 198

Ala Val Leu Ser Asn Val Met Phe Ile
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<400> 199

Gly Asn Tyr Thr Asp Arg Met Phe Ile
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<211> 9

<212> PRT

<213> synthetic enterokinase cleavage sequence

<400> 200

Asp Ile Asn Asp Asp Arg Ser Leu Phe

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5

<210> 201

<211> 9

<212> PRT

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<400> 201

Asn Lys Ala Lys Asp Arg Met Phe Ile

1

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<210> 202

<211> 9

<212> PRT

<213> synthetic enterokinase cleavage sequence

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Gly Asn Tyr Thr Asp Arg Arg Phe Ile

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<210> 203

<211> 9

<212> PRT

<213> commercial synthetic enterokinase cleavage substrate

<400> 203

Gly Asn Tyr Thr Asp Arg Tyr Phe Ile

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<211> 7

<212> PRT

<213> synthetic enterokinase cleavage sequence

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<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa is any amino acid

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<400> 204

Asp Ile Asn Asp Asp Arg Xaa
1 5

<210> 205

<211> 7

<212> PRT

<213> synthetic enterokinase cleavage sequence

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa is any amino acid

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<211> 7

<212> PRT

<213> synthetic enterokinase cleavage sequence

<220>

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<222> (1)..(1)

<223> Xaa1 is an optional amino acid which, if present, is Ala, Asp, Glu, Phe, Gly, Ile, Asn, Ser, or Val

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa2 is an optional amino acid which, if present, is Ala, Asp, Glu, His, Ile, Leu, Met, Gln, or Ser

<220>

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<222> (3)..(3)

<223> Xaa3 is an optional amino acid which, if present, is Asp, Glu, Phe, His, Ile, Met, Asn, Pro, Val, or Trp

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<222> (4)..(4)
<223> Xaa4 is Ala, Asp, Glu, or Thr

<220>
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<222> (7)..(7)
<223> Xaa7 is any amino acid

<400> 206

Xaa Xaa Xaa Xaa Asp Arg Xaa
1 5

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<223> Xaa1 is an optional amino acid which, if present, is Asp or Glu

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<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa2 is an optional amino acid which, if present, is Val

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa3 is an optional amino acid which, if present, is Tyr

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa4 is Asp, Glu or Ser

<220>
 <221> MISC_FEATURE
 <222> (7)..(7)
 <223> Xaa7 is any amino acid

<400> 207

Xaa Xaa Xaa Xaa Glu Arg Xaa
 1 5

<210> 208
 <211> 6
 <212> PRT
 <213> synthetic enterokinase cleavage sequence

<400> 208

Asp Ile Asn Asp Asp Arg
 1 5

<210> 209
 <211> 6
 <212> PRT
 <213> synthetic enterokinase cleavage sequence

<400> 209

Gly Asn Tyr Thr Asp Arg
 1 5

<210> 210
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 <212> PRT
 <213> streptavidin binding sequence

<400> 210

Trp His Pro Gln Phe Ser Ser
 1 5

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<210> 211
 <211> 10
 <212> PRT
 <213> streptavidin binding sequence

<400> 211

Pro Cys His Pro Gln Phe Pro Arg Cys Tyr
 1 5 10

<210> 212
 <211> 1272
 <212> DNA
 <213> Bacteriophage M13mp18

<400> 212
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 gacgacaaaa ctttagatcg ttacgctaac tatgaggggt gtctgtggaa tgctacaggg 180
 gttgtagttt gtactgggtga cgaaactcag tgttacggta catgggttcc tattgggctt 240
 gctatccctg aaaatgaggg tgggtggctct gaggggtggcg gttctgaggg tggcggttct 300
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 atcaaccctc tcgacggcac ttatccgcct ggtactgagc aaaaccccg c taatcctaata 420
 ccttctcttg aggagtctca gcctcttaata actttcatgt ttcagaataa taggttccga 480
 aataggcagg gggcattaac tgtttatacg ggcactgtta ctcaaggcac tgaccccggt 540
 aaaacttatt accagtacac tctgtatca tcaaaagcca tgtatgacgc ttactggaac 600
 ggtaaattca gagactgcgc tttccattct ggctttaatg aagatccatt cgtttgtgaa 660
 tatcaaggcc aatcgtctga cctgcctcaa cctcctgtca atgctggcgg cggctctggt 720
 ggtggttctg gtggcggtc tgaggggtgg ggctctgagg gtggcggttc tgaggggtggc 780
 ggctctgagg gaggcgggtc cgggtggtggc tctggttccg gtgattttga ttatgaaaag 840
 atggcaaacg ctaataaggg ggctatgacc gaaaatgccg atgaaaacgc gctacagtct 900

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gacgctaaag gcaaacttga ttctgtcgct actgattacg gtgctgctat cgatgggttc 960
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 aattcccaaa tggctcaagt cgggtgacggg gataattcac ctttaatagaa taatttccgt 1080
 caatattttac cttccctccc tcaatcgggt gaatgtcgcc cttttgtctt tagcgctggg 1140
 aaaccatatg aattttctat tgattgtgac aaaataaact tattccgtgg tgtctttgcg 1200
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<400> 213

Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser
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His Ser Ala Glu Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu
 20 25 30

Asn Ser Phe Thr Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr
 35 40 45

Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala Thr Gly Val Val Val Cys
 50 55 60

Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu
 65 70 75 80

Ala Ile Pro Glu Asn Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu
 85 90 95

Gly Gly Gly Ser Glu Gly Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp

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100	105	110
Thr Pro Ile Pro Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr		
115	120	125
Pro Pro Gly Thr Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu		
130	135	140
Glu Ser Gln Pro Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg		
145	150	155
Asn Arg Gln Gly Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly		
165	170	175
Thr Asp Pro Val Lys Thr Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys		
180	185	190
Ala Met Tyr Asp Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe		
195	200	205
His Ser Gly Phe Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln		
210	215	220
Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala Gly Gly Gly Ser Gly		
225	230	235
Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly		
245	250	255
Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly		
260	265	270
Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala		
275	280	285

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Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly
290 295 300

Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe
305 310 315 320

Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp
325 330 335

Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn
340 345 350

Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln
355 360 365

Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu
370 375 380

Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala
385 390 395 400

Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala
405 410 415

Asn Ile Leu Arg Asn Lys Glu Ser
420

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<212> DNA

<213> Bacteriophage M13mp18

<400> 214

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ggcacttata cgcttggtac tgagcaaaac cccgctaata ctaatccttc tcttgaggag 120

tctcagcctc ttaatacttt catgtttcag aataataggt tccgaaatag gcagggggca 180

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ttaactgttt atacgggcac tgttactcaa ggcactgacc ccgttaaaac ttattaccag 240
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 tgcgctttcc attctggctt taatgaagat ccattcgttt gtgaatatca aggccaatcg 360
 tctgacctgc ctcaacctcc tgtcaatgct ggcgggcggt ctggtggtgg ttctggtggc 420
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 aaggggggcta tgaccgaaaa tgccgatgaa aacgcgctac agtctgacgc taaaggcaaa 600
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 ctccctcaat cggttgaatg tcgccccttt gtcttttagcg ctggtaaacc atatgaattt 840
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<210> 215
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 <212> PRT
 <213> Bacteriophage M13mp18

<400> 215

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Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro Ala
 20 25 30

Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe Met
 35 40 45

Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val Tyr
50 55 60

Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr Gln
65 70 75 80

Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn Gly
85 90 95

Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro Phe
100 105 110

Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val
115 120 125

Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly
130 135 140

Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly
145 150 155 160

Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met
165 170 175

Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala
180 185 190

Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr
195 200 205

Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn
210 215 220

Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala
225 230 235 240

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Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln
 245 250 255

Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe
 260 265 270

Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn
 275 280 285

Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met
 290 295 300

Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
 305 310 315

<210> 216

<211> 450

<212> DNA

<213> Bacteriophage M13mp18

<400> 216

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gctgctatcg atggtttcat tggtgacggt tccggccttg ctaatggtaa tggtgctact 180

ggtgattttg ctggctctaa ttcccaaagt gctcaagtcg gtgacggtga taattcacct 240

ttaatgaata atttccgtca atatttacct tccctccctc aatcggttga atgtcgccct 300

tttgtcttta gcgctggtaa accatatgaa ttttctattg attgtgacaa aataaactta 360

ttccgtggtg tctttgcgtt tcttttatat gttgccacct ttatgtatgt attttctacg 420

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<211> 150

<212> PRT

<213> Bacteriophage M13mp18

<400> 217

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Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu
 20 25 30

Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly
 35 40 45

Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala
 50 55 60

Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro
 65 70 75 80

Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val
 85 90 95

Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser
 100 105 110

Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu
 115 120 125

Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile
 130 135 140

Leu Arg Asn Lys Glu Ser
 145 150